



The logo for EMBL-EBI (European Bioinformatics Institute) is displayed. It features a circular pattern of small dots in the top left corner, followed by the text 'EMBL-EBI' in large, bold, black letters. Below this, 'European Bioinformatics Institute' is written in a smaller, black, sans-serif font. A navigation bar at the top includes links for 'Get', 'Nucleotide sequences', 'for', 'Site search', 'EBI Home', 'About EBI', 'Research', 'Services', 'Toolbox', 'Databases', 'Downloads', 'Submissions', and 'ANALYSIS TOOLS'.

EBI Generic DB Entry Retrieval

ID AE007337 standard; DNA; PRO; 10216 BP.
XX
AC AE007337; AE005672;
XX
SV AE007337.1
XX
DT 31-JUL-2001 (Rel. 68, Created)
DT 02-SEP-2002 (Rel. 72, Last updated, Version 4)
XX
DE Streptococcus pneumoniae TIGR4 section 20 of 194 of the complete genome.
XX
KW
XX
OS Streptococcus pneumoniae TIGR4
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus;
OC Streptococcus pneumoniae.
XX
RN [1]
RP 1-10216
RX MEDLINE; 21357209.
RX PUBMED; 11463916.
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S.,
RA Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M.,
RA Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O.,
RA Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M.,
RA Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S.,
RA Dickinson T., Hickey E.K., Holt I.E., Loftus B.J., Yang F., Smith H.O.,
RA Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
pneumoniae";
RL Science 293(5529):498-506(2001).
XX
RN [2]
RP 1-10216
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S.,
RA Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M.,
RA Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O.,
RA Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R.,
RA Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Geswan P.,
RA Hickey E.K., Holt I.E., Loftus B.J., Ujwal M.L., Yang F., Smith H.O.,
RA Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT ;
RL Submitted (29-JUN-2001) to the EMBL/GenBank/DDBJ databases.
RL The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD
RL 20850, USA
XX
DR SPTREMBL; Q97SS4; Q97SS4.
DR SPTREMBL; Q97SS5; Q97SS5.
DR SPTREMBL; Q97SS6; Q97SS6.

DR SPTREMBL; Q97SS7; Q97SS7.

DR SPTREMBL; Q97SS8; Q97SS8.

DR SPTREMBL; Q97SS9; Q97SS9.

DR SPTREMBL; Q97ST0; Q97ST0.

DR SPTREMBL; Q97ST1; Q97ST1.

DR SPTREMBL; Q97ST2; Q97ST2.

DR SPTREMBL; Q97ST3; Q97ST3.

XX

FH Key Location/Qualifiers

FH

FT source 1..10216

FT /db_xref="taxon:170187"

FT /organism="Streptococcus pneumoniae TIGR4"

FT /strain="TIGR4"

FT CDS 153..845

FT /codon_start=1

FT /db_xref="SPTREMBL:Q97ST3"

FT /transl_table=11

FT /gene="SP0240"

FT /product="phosphoglycerate mutase family protein"

FT /protein_id="AAK74420.1"

FT /translation="MVKVRLLVVRHGKTMFNTIGRAQGWSDTPLTAEGERGIQELGIGL

FT RESDLQFERAYSSDSGRTIQTMGIILEELGLQGEIPYRMDKRIREWCFGSDGAYDGDL

FT FMGIIIPRIFNVDHVHQLSYELAEGLVEVDTAGWAEGWEKLSGRIKEGFEMIAKEMEDQ

FT GGGNALVVSHGMTIGTIVLINGMHPHLDNGSVTILEYEDGQFRVEVVGDRSYRELGR

FT EKMEEGSI"

FT CDS complement(2583..3674)

FT /codon_start=1

FT /db_xref="SPTREMBL:Q97ST2"

FT /transl_table=11

FT /gene="SP0242"

FT /product="ABC transporter, ATP-binding protein"

FT /protein_id="AAK74421.1"

FT /translation="MSEIKIINAKKIYHDVPIENLNITIPKGSLFTLLGASGCGKTTL

FT LRMIAGFNSIEGGEFYFDDTKINNMEPSKRNIGMFQNYAIFPHLTVRDNVAFGLMQKK

FT VPKEELIQQTQNCKYLELMQIAQYADRKPDKLSSGGQQQRVTLACALAVNPSVLLMDEPLSN

FT LEAKLRLDMRQAIREIQLHEVGITTVYVTHDQEEAMAISDQIAVMKDGVIQQIGRPKELY

FT HKPANEFVATFIGRTNIIIPANLEKRSRGAYIVFSDGYALRMPALDQVEEQAIHVSIRPE

FT EFIGDESGDIEGTIRDSVYLGLNNTDYFIETGFASKIQVSEESTFEEDLQKGNRIRLRIN

FT TQKLNIFSADGSQNLIKGVNHGT"

FT CDS complement(3687..4703)

FT /codon_start=1

FT /db_xref="SPTREMBL:Q97ST1"

FT /transl_table=11

FT /gene="SP0243"

FT /product="iron ABC transporter, iron-binding protein"

FT /protein_id="AAK74422.1"

FT /translation="MKKKWMYYAACSSNESADDSSDKGDGGSLVVYSPNSEGLIGATI

FT PAFEEKYGIKVELIQAGTGEFKKLESEKEPVADVFGGSYTQYTTGELFENYTSKE

FT NDNVIKEYQNTTGYSTPYTLGDSVLIVNPDLTKGMNIEGYNDLFKPELKGKIATADPAN

FT SSSAFAQLTNMLQAQGGYKDDKAWSYVKDLFTLIDKGKIGSSSSSVYKVVADGEMAVGLS

FT YEDPAVKLLNDGANIKVYVPEGTVFLPASAIVKKSKNMENAKKFIDFIISQEVQDTL

FT GTTTTNRPVRKNAKTSENMKPIDKIKTLTEDYDYVIKNKSDIVKKYNEVFTDIQSKQ"

FT CDS complement(5008..5115)

FT /codon_start=1

FT /db_xref="SPTREMBL:Q97ST0"

FT /note="identified by Glimmer2; putative"

FT /transl_table=11

FT /gene="SP0244"

FT /product="hypothetical protein"

FT /protein_id="AAK74423.1"

FT /translation="MSHSFKKSLQKEILHRSSIAAFVTSRAFSDTVSPV"

FT CDS complement(5290..6066)

FT /codon_start=1

FT /db_xref="SPTREMBL:Q97SS9"

FT /note="identified by match to PFAM protein family HMM
FT PF02143"
FT /transl_table=11
FT /gene="SP0245"
FT /product="pyruvate formate-lyase-activating enzyme,
FT putative"
FT /protein_id="AAK74424.1"
FT /translation="MEISKGIIIFIQHFSIHDGPGIRTTVFLKGCPWCSNPESQR
FT MKPEKMKDAQREKFTILVGEETKVEEIITEVLKDKEFYEESGGLTLSGGEIFAQFEFAK
FT AILKSAKEHHIHTAIETTAFVDHEKFIDLIQYVDFIYTDLKHYNSIKHKKVTGVFNQMI
FT IKNIHYAFSQNKTVILRIPVIPNPNNSLEDAEKFATLFLNSLNIDQVQLPFHQFGENKY
FT RLLNRKYEMDGINALHPEDLIDYQKVFLNHHINCYF"
FT CDS
FT 6188..6934
FT /codon_start=1
FT /db_xref="SPTREMBL:Q97SS8"
FT /transl_table=11
FT /gene="SP0246"
FT /product="transcriptional regulator, DeoR family"
FT /protein_id="AAK74425.1"
FT /translation="MKRLEQI I KLVSEYEKIDVNTLSEKLNVS KVTIRKDLDKLESKGL
FT LHREHGYAVLNSGDDLNVRSL SINYETKRKIVQEAVKLVSDNETIMIESGSTCALLAEEI
FT CKQKRNVTIVTNSFFIANFVRAYDSCRVIVLGGEFQKDSQVTVGPLLKEMIQTTFHVCQA
FT FVGTGDGYDKEMGFTGKDLMRSEVVQYISAVSDKIVLTDSSKFDKRGTVRRFALSQVYE
FT VITDEKLSKQNIATLENAGIMVKVVS"
FT CDS
FT 6947..7927
FT /codon_start=1
FT /db_xref="SPTREMBL:Q97SS7"
FT /note="similar to SP:P37078 GB:X66059 PID:43938; identified
FT by sequence similarity; putative"
FT /transl_table=11
FT /gene="SP0247"
FT /product="transcriptional regulator"
FT /protein_id="AAK74426.1"
FT /translation="MNQDRNKLLSKIA YLYYIENLNQS QIAAKLGIYRTSISRMLTEAR
FT NVGIVKIEIENFDTNMFKLEN YVKEK SLES IIPNEFDDTPTILSERISQVAAGVLR
FT NLIDDNMKIGFSWGKSLNLDLHSKSVRNHFYPLAGGPHI HAKYHVNTL IYEMSR
FT KFHGECTFMNATIVQENKLLADGILQ SRYFENLKN SWKLDIAVVGIGDFSNKGKHQWL
FT DMLTEDDFKELTKVKTGEICC RFFDSKGKEVYENLQERTIAISLEDLKNIPQSLAVAY
FT GDTKVSSILS VLRANLVNHLITDKNTILK VLEEDGDLT FREILGE"
FT CDS
FT 8122..8442
FT /codon_start=1
FT /db_xref="SPTREMBL:Q97SS6"
FT /transl_table=11
FT /gene="SP0248"
FT /product="PTS system, IIA component"
FT /protein_id="AAK74427.1"
FT /translation="MEMIVPDQIIMGLILYAGDAKQHIYKALDYIKNGTCERCEEEIQL
FT ADAALLEAHNLQTKFLAQEASGTKEITALFVHSQDHLM TSMTEINLIKEIISLRKELH
FT KK"
FT CDS
FT 8488..8796
FT /codon_start=1
FT /db_xref="SPTREMBL:Q97SS5"
FT /transl_table=11
FT /gene="SP0249"
FT /product="PTS system, IIB component"
FT /protein_id="AAK74428.1"
FT /translation="MVKIGLFCAAGFSTGMLVNNMKIAAQSSGVEAEIEAFSQSKLADY
FT APNIDVALLG P QVAYTLDKSKEICDKCDVPIAVIPMMDYGM LDGKKVLDLALS LISG"
FT CDS
FT 8789..10111
FT /codon_start=1
FT /db_xref="SPTREMBL:Q97SS4"
FT /transl_table=11
FT /gene="SP0250"
FT /product="PTS system, IIC component"
FT /protein_id="AAK74429.1"

/translation="MGKKRRFIMS KMDVQKIIAPMMKFVNMRGIIIAKLDGMLAILPLTV
 VGSLFLIMGQLPFEGLNKSIAVFGANWTEPFM QVYSGTFAIMGLISCFSIAYS YAKNS
 GVEALPAGVLSVSAFFILLR SSYIPKQGEAIGDAIS KVWFGGQGIIGAIIGLVVGSIY
 TFFIKRKIVIKMPEQVPOAIAKOFTEAMIPAFVIFLSSMIVYI LAKSLTNGGTFIEMIYS
 AIQVPLQGLTGSILYGAIGIAFFISFLWWFGVHGQSVVNGVVTALLS NL DANKAM LASA
 NLSLENGAHIVTQQFLDSFLILSGSGITFGLVVAMLF AAKSKQYQALGKVAAPAI FNV
 NEPVVFGFPIVMNPVMFV PFLIPVLA AVIVYGAIA TGF M QPFS GVTLPWSTPA ILSGF
 LVGGWQGVITQLVILAMSTLVYFPFFKQDRLAYQNEIKQS"

Sequence 10216 BP; 3252 A; 1519 C; 2088 G; 3357 T; 0 other;

aacactgaat	60
tagtttgaat	
ttgat tttca	
tctaataatct	
ttat ttaatg	
aactcctaaa	
ctttttcata	120
ataatctcct	
tcaaaagtcg	
cctgtatggg	
tggctttat	
ttatcatc	
atgatataat	180
agaagcaa ac	
ggaggacgga	
aaatggtaaa	
agtacgattt	
tatttggta	
gtcatggcaa	240
gaccatgtt	
aacacgattt	
gtcgcgcga	
aggttggagc	
gataactcc	
taactgctga	300
aggtgaacga	
gggattcaag	
agtttaggaat	
cggtttgcga	
gaatctgatc	
tacagttga	360
gcgtgctt at	
tcgagtgatt	
ctggcgtac	
cattcagacc	
at tgggatta	
tccttgaaga	420
acttggctt	
cagggggaaa	
tccctt atcg	
atgggtttt	
cggtagttt	
gatggagcct	
atgatggcga	
tctcgatc t	480
taatgtggac	
cacgtt cacc	
aatttgc tta	
tggttagagg	
cgatacagct	540
ggttggctg	
aaggctggg	
atggaggc tt	
tgaaatgatt	
gcaaaagaaa	
tggaagatc	
ttgtcagcca	600
t ggaatgact	
attggaaacca	
ttgtt atct	
atggcttgg	
taatgtggac	
gtgacaatcc	
ttgaatatga	
aagttgtcgg	720
tgaccgtat	
taccgagagc	
taggacgtga	
tttaatcagt	
ctagacttgc	
ttgccc atgag	
ctagggattt	
aaaaaacagc	780
cgagggcact	
cctt cggct	
gtt tttgat	
ctattgctt	
tagagattt	
cataaacaag	
agcaaggaa	
atagttgaca	840
aggttgcggc	
tacaccgtaa	
tttccctctg	
acagtcat	
ttcttgc tttt	900
gacattgtt	
aggaggatag	
attgtgactc	
aagataagat	
ggctccagaa	
atgataccag	
atcttagcaa	960
aggtatttgc	
acgactactt	
cctaagctt	
ggtgc tattt	1020
gtt gtaagct	
agcaacagat	
gagcgaatag	
gatagagaca	
taatcaagat	
gaaagcagtc	
cctgtatc	
agaccagtt	1080
tgaaggaa	
aatgaaggca	
atccctagaa	
ggtaccatac	
tgaggctgtc	
aattaatgtt	
gtaaacaaat	
taggagataa	1140
atgtcgc aaa	
tagaacaact	
agaactaagg	
gtattt gaaa	
tagcagatcc	
catacgtat	
aaagcttac	
cctttaacag	1200
ataccatacc	
tgatgtttt	
aggaaagagg	
ggtaaaacag	
agataaagat	
aatttccgtat	
actgttgc	
tttgc tagttt	1260
ttttaggctc	
aatttggat	
agcagattca	
gcaatgtgtt	
tttggataag	
gaaaatttgc	
aaggcaatga	
gcagaatttc	1320
ctccaaacctc	
gctaataat	
tgggtataaa	
tacccttcg	
caatcaacat	
aggcgttcca	
aagtctgaga	
tttgc tagttt	1380
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
agaccaggat	
aatggcata	
tttgc tagttt	1440
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	1500
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	1560
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	1620
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	1680
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	1740
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	1800
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	1860
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	1920
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	1980
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	2040
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	2100
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	2160
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	2220
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	2280
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	2340
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	2400
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	2460
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	2520
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	2580
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	2640
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	2700
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	2760
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	2820
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	2880
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	2940
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	3000
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	3060
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	3120
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	3180
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	3240
ttttaggctc	
aatttggat	
agcagattca	
gaaagcagtc	
cctgtatc	
atcccttgc	
tttgc tagttt	3300

tgagcaattt	gcatgaggttc	aagatacttg	ttggtctgtt	gaatcaattc	ttctttgga	3360
accttcttt	gcataagacc	aaaagcaacg	ttgtctcgga	cagtcaaattg	tggaaaata	3420
gcgtagttt	ggaaaaccat	cccgatattg	cgttgcgtgg	gttccatatt	attgattttt	3480
gtatcatgca	agtaaaattc	tccacccatcg	atactgttg	aacctgcaat	catacgaaga	3540
agggtcgtt	tcccacatcc	tgaagctcca	agaagggtaa	agagacttcc	ttttggaatt	3600
gtaatgttca	aattctcaat	aacagggaca	tcgtggtaga	ttttttggc	gttaataatt	3660
ttgatctcac	tcatagtgaa	cctcttttac	tgttttagatt	ggatatctgt	aaagacttcg	3720
ttgtatttct	taacgatatac	tgatttattc	ttgatgacat	aatcataatc	ttcagtgagt	3780
gtttttagtt	tgtcaatttgg	tttcatgttt	tcgcgtgttt	tagcattttt	acgaacacgga	3840
cggtagtag	tgggtgtacc	aagtgtatct	tgtacttctt	gagagataat	aaaatcgata	3900
aatttcttgg	cattttccat	attttagat	ttttaacga	tagcagcact	agcaggtagg	3960
aagacggttc	cttcttttgg	atagactacc	ttaatgttag	ctccgtcatt	taagagttt	4020
actgctggat	cttcataaga	gagaccaaca	gccatttctc	catcagcgac	tactttatag	4080
acactagatg	aacttgaacc	gattttacca	tcaataagt	tgaaaagatc	ttttacataa	4140
gaccaagcct	tatcatctt	gtaaccacct	tgagcttga	gcatatttgc	taattgagca	4200
aaggcgctag	aagagtttgc	tgggtcagca	gttgcgattt	ttccttttag	ttcagggttt	4260
aaaagatcg	tatattccctc	gatgttcatg	ccttttagta	aatcagggtt	gacgattaaa	4320
acactaccat	ctagtgtata	aggagtagag	tagccagtt	tgtttgata	ttctttgata	4380
acatttatcat	tttcttttga	agtagatgtt	tcaaagagtt	ctccgtgggt	agtatattgt	4440
gtataagaac	caccaaagat	aacatcagct	acaggaactt	cttttctga	ctctagttt	4500
ttgaaaagtt	ctccagttacc	agcttgaatc	agttctactt	tgataaccata	tttttcttca	4560
aaggcaggaa	tagttgtcc	aattaagccc	tctgagttt	gtgaataaaac	gactagcgaa	4620
ccggcgtctc	ctttatcaga	tgaactgtca	tcggcagatt	cattagaaga	acaagcagca	4680
taatacatcc	atttctttt	catgtatggat	acctccgtt	tgttatttaa	gtttattttt	4740
aaacaatgta	agcgttttta	aaacatacaa	ttcttattcta	tagtgtattt	aatctataac	4800
agtacacttt	gactgctaaa	atatttctat	aaattaattt	gactttcctg	atagagatgt	4860
tcacatctta	tttcaattca	ctatatttga	gtaaaattct	ctacaaaaag	aagaatagcc	4920
tattttacta	ttcttctttag	tgatttcaat	tcctttgggg	aaatatggag	atacttttta	4980
aatcctgaca	aatggtttgg	tcttttctt	aatcggttgc	actgtatcgg	agaatgcgcg	5040
tgaggtcaca	aaggctgcga	tagagcttct	atggagaatt	tcttttggg	gagatttttt	5100
aaaggaatga	gacatccgct	accccttgg	aaggttttt	tgtgataagt	atagcagttt	5160
aaaaattctt	gagcaaggta	aaatagaaaa	ggtttggcta	aaatttttta	gctaaacctt	5220
ttgaaaagtt	aagtatgtat	tatagatgt	tgttattctgc	aaatagctag	agcatttcaa	5280
ggaaataaaac	tagaaataac	aattaatatg	gtggttcaga	aatacctttt	gataatcaat	5340
aagatcttca	ggatgaagt	cgttgattcc	atccatttca	tatttccgat	ttaataaacg	5400
atatttgttt	tcaccaaattt	gatggaaagg	gagtagttga	acttggtcga	tatttataatga	5460
gttaaataga	gtagcgaatt	tttctgcattc	ctctaaacta	tgtttaaaaat	taggataaac	5520
tgggatttctt	aaaacgatag	tttttatttt	tggaaaagca	taatgaatgt	ttttataataat	5580
catttgatta	aaaaccccg	tcactttttt	atgtttata	gaattataat	gttttaggtc	5640
tgttagata	aaatccacat	attgaattaa	atcaataaaat	tttcatgat	caacaaaggc	5700
agtagttca	atggcagtgt	gtatgtatg	ttcttttagct	gattttttaaga	tggctttagc	5760
aaattcaaac	tgagcaaata	tttcacccctc	tgataaagtt	aaacctccac	cggatttctc	5820
gtaaaattct	ttgtcttttta	atacctctgt	aataatttct	tctacagtct	tttcttcacc	5880
gactaagggt	aatttctctc	gttgagcatc	tttcattttt	tcaggtttca	ttctttgaga	5940
ttcaggattt	gaacaccatg	gacagcgccag	aggacatcct	ttttaaaaaaa	cagttgtacg	6000
aatacccgga	ccgtcatgaa	ttgaaaagtg	ttgaatattt	aaaataattt	cttttagat	6060
ttccataaga	gttccttcctc	ttcataagtc	tatcctatca	caaaaacgaa	agaaaaacaa	6120
ttacgaacga	aaggtaattt	tgttggttt	tgctttttat	tttggtagaa	taaaacggag	6180
gtgtaaaatg	aaaagattgg	aacaaattat	taaatttagta	tcagaatatg	aaaagatcga	6240
cgttaataca	ttatcgaaaa	aattaaatgt	atcgaaagta	acgatttagaa	aagatttaga	6300
taaatttagag	tcaaaaagg	tattacacag	agagcatgga	tatgtgtat	taaattagtgg	6360
agatgactt	aatgtacgtt	tgtcaattaa	ttatgaaact	aaagaaaaaa	ttgttcaggaa	6420
agcagtaaaa	ttgggtgtcag	ataatgaaac	aataatgata	gaatctggat	cgacctgtgc	6480
tttacttgc	gaggaaattt	gcaagcaaaa	aagaaatgtt	acgattgtaa	caaattcggt	6540
ttttatagca	aattttgtga	gagcttatga	ttcatgtcgt	gttatttttc	ttgggtgtga	6600
gtttcagaaa	gattcacagg	tgactgttag	accttttattt	aaagaaatgt	tacagacttt	6660
tcatgtgtgt	caagctttt	ttggggacaga	tggttacgt	aaagagatgg	gctttaccgg	6720
aaaagattt	atgcgcagtg	aggtagttca	atatatttca	gcagtgtcgg	ataaaagtcat	6780
tgtcctaact	gactcaagta	aatttgataa	aagaggta	gtaagaagat	ttgcttaag	6840
tcaagtctat	gaagtaataa	cagacgaaaa	actttctaaa	caaataataat	ctacatttata	6900
aaatgtctgg	ataatggta	aggtatgtt	gtaagaggtt	aagtgtatgt	atcaagatag	6960
gaataaaactg	ctttctaaaa	ttgttttatct	gtattatattt	gaaaactttaa	atcagtcaca	7020
aatacgacgca	aaatttaggaa	tttatagaaac	ctcttattatgt	agaatgtttaa	cagaagcaag	7080
gaatgttagga	attgttaaaa	ttgaaaataga	gaattttgtat	accaatatgt	ttaagggttga	7140
aaattatgtt	aaagaaaaat	acagtttgg	aagtttagaa	attattccaa	atgaattttga	7200

tgatactcca	acaattttat	ctgaaagaat	ttctcaagtt	gcagcaggcg	tccttaggaa	7260
tctaatttat	gataatatga	aaattggctt	ttcttggggg	aaaagtttaa	gtatattgt	7320
agatttaatt	cacagtaaaa	gtgtccgaaa	tgttcaacttc	tatcctctag	caggtggtcc	7380
tagtcacata	cacgcttaat	accatgtgaa	tacactgatt	tatgaaatgt	ctagaaaatt	7440
tcatggagag	tgtacattta	tgaatgcaac	gattgtgca	gaaaataaaat	tgttagcaga	7500
tggtattttg	caatcaagat	atttgaaaaa	tttggaaaaat	agttggaaag	atttagat	7560
agctgttagtc	ggaattgggt	attttagcaa	taaaggaaaa	catcaatggt	tagacatgct	7620
tacagaggat	gactttaaag	aattgaccaa	agttaaaact	gttaggagaaa	tttgggtcg	7680
atttttgtat	tcaaaaaggta	aagaagtcta	tgaaaactta	cagggaaagaa	cgatagcaat	7740
ctctttggaa	gatttaaaaaa	atattccctca	aagtttagct	gttgcttacg	gtgatcacaa	7800
agtatctcg	attcttctg	tcttcgtgc	taattttagta	aatcatttga	ttacagacaa	7860
aaatacaatt	ttaaaaagttt	tggaaagaaga	tggggatttt	acttttagag	agattctagg	7920
tgagtaaaaa	tgatagactg	attcagtta	tcgtttttct	ttttagttga	ttgcacattt	7980
gtgcttatat	aaacaaaaat	agtttatctg	ttgtttttgg	attgacaact	ttattatgt	8040
gttgtattct	atagttacaa	aagaaaattt	taaaattca	aatgaaaaaa	gttttttaca	8100
tagtgaatgt	aggaggaatt	tatggaaatg	attgttccag	atcaaattat	catgggttta	8160
attttatatg	ctgggtatgc	gaaacaacat	atttataaag	cgtaggat	cataaaaaat	8220
ggtacatgtg	aacgggtgtga	agaagaaata	cagttagctg	atgcagcctt	attagaagct	8280
cataatctac	aaacaaaattt	tttggcacag	gaagcgtctg	gtacaaagac	agaaattaca	8340
gctcttttg	ttcatttcaca	agatcatctc	atgaccagta	tgacggagat	taatttaatc	8400
aaagaaattta	ttagttttag	aaaagaactt	cataaaaaat	aatactagag	tattatcatt	8460
gttattaaca	tagaggagga	aaacataatg	gtgaagattt	ttttgtttt	tgcagcaggt	8520
ttttctactg	gtatgcttgt	aaataatatg	aaaattgcag	cgcaatctag	tggagtttag	8580
gcagaaatag	aggcggtttc	tcagtctaaa	ttagcggatt	atgcgc当地	tatagatgtt	8640
gcactattgg	gtccacaagt	tgcttataca	ttagataat	caaaagaaat	ttgtgataag	8700
tgtgtatgtc	cgatagctgt	tattccgtat	atggactat	gtatgttag	tggaaaaaaa	8760
gtattagatt	tggccctatc	ttttagttgt	gggtaagaaa	aggagattt	ttatgtcaaa	8820
gatggatgtt	cagaaaatca	ttgcaccgt	gatgaagttt	gtgaatatgc	gtggcattat	8880
agctctaaaa	gatgggatgt	tagcaatttt	gccattgaca	gtagttggta	ttttgttctt	8940
gattatggga	caattggccgt	tcgaaggatt	aaataagagc	attgctagtg	tttttgagc	9000
taattggaca	gagccgttta	tgcaagtata	ttcaggaact	tttgcattt	tgggtctaat	9060
ttcttggttt	tcaattgcct	attcttatgc	taagaatagc	ggagtagagg	ctttaccagc	9120
tggagttcta	tctgtatctg	cattcttat	tttgcttaaga	tcatcttata	tccctaaaca	9180
aggtgaggcg	atggggacg	ctattagtaa	agtttggttt	ggaggccaag	gaattatcg	9240
tgctatcatt	ataggtttgg	tagtaggaag	tatttatacc	ttctttataaa	agagaaaaat	9300
tgtttataag	atgccagaac	aagttccaca	agctattgc	aaacagttt	aagcaatgt	9360
tccagcatt	gtatatttct	tatcttctat	gattgtat	attttagcga	agtcattgac	9420
taatggcgg	acattcatag	aaatgattta	ttctgcatt	caagttccgt	tgcaaggttt	9480
aactggatct	ttgtatgg	ctattggat	tgcattctt	atatcattt	tgtgggtt	9540
tgggttcat	gggcaatcg	tagtaaatgg	agtagtgaca	gctctgc	tatctaatct	9600
tgatgctaat	aaagctatgt	tagcctctgc	taatctatca	ttagaaaatg	gtgcacat	9660
tgttactcaa	caatttttag	attcattttt	aattctatca	ggttcaggga	ttacgtttgg	9720
tctttagtt	gccatgc	ttgcagcaaa	atcaaaca	taccaagc	ttggaaaatg	9780
tgcagcttt	ccagcaat	ttaacgtaaa	tgagccagtt	gtatgttgat	ttccgattgt	9840
catgaatcca	gttatgtt	taccttcat	tcttggcc	gtacttgca	ctgtgatagt	9900
atatggagct	attgcaacag	gtttcatgca	gccattctca	ggggtaacat	tgccctggag	9960
tacaccagct	attttatcag	gattttgg	gggtggatgg	caaggagtt	ttactcagct	10020
ggtgatattt	gcgtatgtct	cattgg	tttccattc	tttaaagtac	aggatcg	10080
agcttacca	aatgaaatca	aacaatctt	gaggtattt	tgtgtact	ttaaactc	10140
acatttgc	taaaaattag	agagttaaa	ttttctagt	taaaagctt	aaaatttct	10200
taaaaaatcg	tattat					10216

//

Please contact support@ebi.ac.uk with any problems or suggestions regarding this site.

General information

Entry name	Q97ST2
Accession number	O97ST2
Created	TrEMBLrel. 18, 1-OCT-2001
Sequence update	TrEMBLrel. 18, 1-OCT-2001
Annotation update	TrEMBLrel. 21, 1-JUN-2002

Description and origin of the Protein

Description	ABC transporter, ATP-binding protein.
Gene name(s)	SP0242.
Organism source	Streptococcus pneumoniae.
Taxonomy	Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales; Streptococcaceae; Streptococcus.
NCBI TaxID	1313

References

- [1] Tettelin,H., Nelson,K.E., Paulsen,I.T., Eisen,J.A., Read,T.D., Peterson,S., Heidelberg,J., DeBoy,R.T., Haft,D.H., Dodson,R.J., Durkin,A.S., Gwinn,M., Kolonay,J.F., Nelson,W.C., Peterson,J.D., Umayam,L.A., White,O., Salzberg,S.L., Lewis,M.R., Radune,D., Holtzapple,E., Khouri,H., Wolf,A.M., Utterback,T.R., Hansen,C.L., McDonald,L.A., Feldblyum,T.V., Anguoli,S., Dickinson,T., Hickey,E.K., Holt,I.E., Loftus,B.J., Yang,F., Smith,H.O., Venter,J.C., Dougherty,B.A., Morrison,D.A., Hollingshead,S.K., Fraser,C.M., **Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.** (2001) *Science* **293**:498-506

Position	SEQUENCE FROM N.A.
Comments	STRAIN=TIGR4;
Medline	21357209
PubMed	11463916

Database cross-references

EMBL	AE007337 ; AAK74421.1 ; -.
TIGR	SP0242 ; -.
InterPro	IPR003593 ; AAA_ATPase. IPR003439 ; ABC_transportr.
Pfam	PF00005 ; ABC_tran; 1.
ProDom	PD000006 ; ABC_transportr; 1.
SMART	SM00382 ; AAA; 1.
PROSITE	PS00211 ; ABC_TRANSPORTER; 1.

Keywords

ATP-binding; Complete proteome;

Sequence information

Length: 363 aa, molecular weight: 40757 Da, CRC64 checksum: 3D9F10B1D8DD7731

MSEIKIINAK	KIYHDVPVIE	NLNITIPKGS	LFTLLGASGC	GKTTLLRMIA	GFNSIEGGF	60
YFDDTKINNM	EPSKRNIGMV	FQNYAIFPHL	TVRDNVAFGL	MQKKVPKEEL	IQQTNKYLEL	120
MQIAQYADRK	PDKLSGGQQQ	RVTLACALAV	NPSVLLMDEP	LSNLEAKLRL	DMRQAIREIQ	180
HEVGITTVYV	THDQEEAMAI	SDQIAVMKDG	VIQQIGRPKE	LYHKPANEJV	ATFIGRTNII	240
PANLEKRSRG	AYIVFSDGYA	LRMPALDQVE	EQAIHVSIRP	EEFIKDESGD	IEGTIRDSVY	300
LGLNTDYFIE	TGFASKIQVS	EESTFEEDLQ	KGNRIRRLIN	TQKLNIFSAD	GSQNLIKGVN	360
HGT						363

//

[General](#) [Description](#) [References](#) [Links](#) [Keywords](#) [Sequence](#)